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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/004,832

DATE: 12/14/2001
TIME: 10:10:15

Input Set : A:\pf105pld2.ST25.txt
Output Set: N:\CRF3\12142001\I004832.raw

ENTERED

#2

3 <110> APPLICANT: Kirkness et al.
5 <120> TITLE OF INVENTION: Human Haemopoietic Maturation Factor
7 <130> FILE REFERENCE: PF105P1D2
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/004,832
C--> 9 <141> CURRENT FILING DATE: 2001-12-07
9 <150> PRIOR APPLICATION NUMBER: US 09/333,033
10 <151> PRIOR FILING DATE: 1999-06-15
12 <150> PRIOR APPLICATION NUMBER: US 08/442,497
13 <151> PRIOR FILING DATE: 1995-05-16
15 <150> PRIOR APPLICATION NUMBER: US 08/187,186
16 <151> PRIOR FILING DATE: 1994-01-25
18 <160> NUMBER OF SEQ ID NOS: 9
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 600
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (46)..(474)
30 <223> OTHER INFORMATION:
33 <400> SEQUENCE: 1
34 agacagcggga actaagaaaa gaagaggcct gtggacagaa caatc atg tct gac tcc 57
35 Met Ser Asp Ser
36 1
38 ctg gtg gtg tgc gag gta gac cca gag cta aca gaa aag ctg agg aaa 105
39 Leu Val Val Cys Glu Val Asp Pro Glu Leu Thr Glu Lys Leu Arg Lys
40 5 10 15 20
42 ttc cgc ttc cga aaa gag aca gac aat gca gcc atc ata atg aag gtg 153
43 Phe Arg Phe Arg Lys Glu Thr Asp Asn Ala Ala Ile Ile Met Lys Val
44 25 30 35
46 gac aaa gac cgg cag atg gtg gtg ctg gag gaa gaa ttt cag aac att 201
47 Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe Gln Asn Ile
48 40 45 50
50 tcc cca gag gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc 249
51 Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe
52 55 60 65
54 gtg gtt tac agc tac aag tac gtg cat gac gat ggc cga gtg tcc tac 297
55 Val Val Tyr Ser Tyr Lys Tyr Val His Asp Asp Gly Arg Val Ser Tyr
56 70 75 80
58 cct ttg tgt ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa 345
59 Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln
60 85 90 95 100
62 cag atg atg tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag 393
63 Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu
64 105 110 115
66 ctc aca aag gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc 441

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67 Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala
68          120          125          130
70 tgg ctc caa gaa aag ttg tct ttc ttt cgt tga tctctgggct ggggactgaa      494
71 Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
72          135          140
74 ttcctgatgt ctgagtcctc aaggtgactg gggacttgga acccctagga cctgaacaac      554
76 caagacttta aataaatttt taaatgcaaa aaaaaaaaaa aaaaaa      600
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 142
81 <212> TYPE: PRT
82 <213> ORGANISM: Homo sapiens
84 <400> SEQUENCE: 2
86 Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu Leu Thr Glu
87 1          5          10          15
90 Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn Ala Ala Ile
91          20          25          30
94 Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu
95          35          40          45
98 Phe Gln Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg
99          50          55          60
102 Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val His Asp Asp Gly
103 65          70          75          80
106 Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys
107          85          90          95
110 Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val
111          100          105          110
114 Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp
115          115          120          125
118 Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
119          130          135          140
122 <210> SEQ ID NO: 3
123 <211> LENGTH: 93
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Contains a BspHI restriction enzyme site and the ompA leader
sequ
129          ence.
131 <400> SEQUENCE: 3
132 gacttcatga aaaagacaga tatcgcaatt gcagtggcac tggctgggtt cgctaccgtt      60
134 gcgcaagctg cttctgactc cctgggtggtg tgc      93
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 31
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Contains complementary sequences to a BglII site.
145 <400> SEQUENCE: 4
146 gactagatct acgaaagaaa gacaactttt c      31
149 <210> SEQ ID NO: 5

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150 <211> LENGTH: 35
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Contains a HindIII site.
157 <400> SEQUENCE: 5
158 gactaagctt agccatgtct gactccctgg tgggtg                      35
161 <210> SEQ ID NO: 6
162 <211> LENGTH: 64
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Contains complementary sequences to an XbaI site,
translation sto
168     p codon, and an HA tag.
170 <400> SEQUENCE: 6
171 gacttctaga tcaagcgtag tctgggacgt cgtatgggta acgaaagaaa gacaactttt      60
173 cttg                                                                64
176 <210> SEQ ID NO: 7
177 <211> LENGTH: 35
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site followed by 6
nucleotide
183     s resembling an efficient signal for the initiation of translatio
184     n in eukaryotic cells (Kozak, M., J. Mol. Biol., 196:947-950 (198
185     7)).
187 <400> SEQUENCE: 7
188 cgcgggatcc gccatcatgt ctgactccct ggtgg                      35
191 <210> SEQ ID NO: 8
192 <211> LENGTH: 30
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Contains the cleavage site for the restriction endonuclease
Asp71
198     8.
200 <400> SEQUENCE: 8
201 gcgcggtacc agtccccagc ccagagatca                      30
204 <210> SEQ ID NO: 9
205 <211> LENGTH: 141
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 9
211 Met Ser Glu Ser Leu Val Val Cys Asp Val Ala Glu Asp Leu Val Glu
212 1           5           10           15
215 Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asn Asn Ala Ala Ile
216           20           25           30
219 Ile Met Lys Ile Asp Lys Asp Lys Arg Leu Val Val Leu Asp Glu Glu
220           35           40           45
223 Leu Glu Gly Ile Ser Pro Asp Glu Leu Lys Asp Glu Leu Pro Glu Arg

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224	50					55					60					
227	Gln	Pro	Arg	Phe	Ile	Val	Tyr	Ser	Tyr	Lys	Tyr	Gln	His	Asp	Asp	Gly
228	65					70					75					80
231	Arg	Val	Ser	Tyr	Pro	Leu	Cys	Phe	Ile	Phe	Ser	Ser	Pro	Val	Gly	Cys
232						85				90					95	
235	Lys	Pro	Glu	Gln	Gln	Met	Met	Tyr	Ala	Glu	Ser	Lys	Asn	Lys	Leu	Val
236				100					105					110		
239	Gln	Thr	Ala	Glu	Leu	Thr	Lys	Val	Phe	Glu	Ile	Arg	Asn	Thr	Glu	Asp
240			115					120					125			
243	Leu	Thr	Glu	Glu	Trp	Leu	Arg	Glu	Lys	Leu	Gly	Phe	Phe			
244		130					135					140				

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date